

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/230,614 A
Source: LFWD
Date Processed by STIC: 11/5/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/05/2004

PATENT APPLICATION: US/10/730,614A

TIME: 10:30:38

Input Set : A:\9_263 seq list 10.25.04.ST25.txt

Output Set: N:\CRF4\11052004\J730614A.raw

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3 <110> APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
4     LI, Jun
5     LI, Xiang
6     YANG, Jianfei
7     MARCU, Kenneth
9 <120> TITLE OF INVENTION: Methods for Modulating IKK ALPHA Activity
11 <130> FILE REFERENCE: 9-263
13 <140> CURRENT APPLICATION NUMBER: US 10/730,614A
14 <141> CURRENT FILING DATE: 2003-12-08
16 <150> PRIOR APPLICATION NUMBER: 60/431,825
17 <151> PRIOR FILING DATE: 2002-12-09
19 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2238
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 ctgggcaccg gcggttcgg gaacgtctgt ctgtaccagc atcggaact tgatctcaaa      120
33 atagcaatta agtcttctcg cctagagcta agtaccaaaa acagagaacg atggtgccat      180
35 gaaatccaga ttatgaagaa gttgaacct gccaatgttg taaaggcctg tgatgttcct      240
37 gaagaattga atattttgat tcatgatgtg cctcttctag caatggaata ctgttctgga      300
39 ggagatctcc gaaagctgct caacaaccca gaaaattgtt gtggacttaa agaaagccag      360
41 atactttctt tactaagtga tatagggtct gggattcgat atttgcata aaacaaaatt      420
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49 actgttgatt attggagctt tgggaccatg gtatttgaat gtattgctgg atataggcct      660
51 tttttgcata atctgcagcc atttacctgg catgagaaga ttaagaagaa ggatccaag      720
53 tgtatatatt catgtgaaga gatgtcagga gaagttcggg ttagtagcca ttacctcaa      780
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57 aattgggacc ctcagcagag aggaggacct gttgacctta ctttgaagca gccaagatgt      900
59 tttgtattaa tggatcacat tttgaatttg aagatagtac acatcctaaa tatgacttct      960
61 gcaaagataa tttcttttct gttaccacct gatgaaagt ctcattcact acagtctcgt      1020
63 attgagcgtg aaactggaat aaatactggg tctcaagaac ttctttcaga gacaggaatt      1080
65 tctctggatc ctcggaaccc agcctctcaa tgtgttctag atggagttag aggctgtgat      1140
67 agctatatgg tttatttgtt tgataaaagt aaaactgtat atgaagggcc atttgcttcc      1200
69 agaagtttat ctgattgtgt aaattatatt gtacaggaca gcaaaatata gcttccaatt      1260
71 atacagctgc gtaaagtgtg ggctgaagca gtgcactatg tgtctggact aaaagaagac      1320
73 tatagcaggc tctttcaggg acaaaggcca gcaatgttaa gtcttcttag atataatgct      1380
75 aacttaacaa aaatgaagaa cactttgatc tcagcatcac aacaactgaa agctaaattg      1440
77 gagttttttc acaaaagcat tcagcttgac ttggagagat acagcgagca gatgacgtat      1500

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79 gggatatctt cagaaaaaat gctaaaagca tggaaagaaa tggaaagaaa ggccatccac 1560
81 tatgctgagg ttggtgtcat tggataacctg gaggatcaga ttatgtcttt gcatgctgaa 1620
83 atcatggagc tacagaagag cccctatgga agacgtcagg gagacttgat ggaatctctg 1680
85 gaacagcgtg ccattgatct atataagcag ttaaaacaca gaccttcaga tcactcctac 1740
87 agtgacagca cagagatggg gaaaatcatt gtgcacactg tgcagagtca ggaccgtgtg 1800
89 ctcaaggagc tgtttggtca tttgagcaag ttgttgggct gtaagcagaa gattattgat 1860
91 ctactcccta aggtggaagt ggccctcagt aatatcaaag aagctgacaa tactgtcatg 1920
93 ttcatgcagg gaaaaaggca gaaagaaata tggcatctcc ttaaaattgc ctgtacacag 1980
95 agttctgccc ggtcccttgt aggatccagt ctagaagggtg cagtaacccc tcagacatca 2040
97 gcatggctgc ccccgacttc agcagaacat gatcattctc tgtcatgtgt ggtaactcct 2100
99 caagatgggg agacttcagc acaaatgata gaagaaaatt tgaactgcct tggccattta 2160
101 agcactatta ttcatgaggc aaatgaggaa cagggaata gtatgatgaa tcttgattgg 2220
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106 <210> SEQ ID NO: 2

107 <211> LENGTH: 21

108 <212> TYPE: DNA

109 <213> ORGANISM: Homo sapiens

112 <220> FEATURE:

113 <221> NAME/KEY: misc_feature

114 <222> LOCATION: (20)..(21)

115 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)

117 <400> SEQUENCE: 2

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121 <210> SEQ ID NO: 3

122 <211> LENGTH: 21

123 <212> TYPE: DNA

124 <213> ORGANISM: Homo sapiens

127 <220> FEATURE:

128 <221> NAME/KEY: misc_feature

129 <222> LOCATION: (20)..(21)

130 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)

132 <400> SEQUENCE: 3

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136 <210> SEQ ID NO: 4

137 <211> LENGTH: 21

138 <212> TYPE: DNA

139 <213> ORGANISM: Homo sapiens

142 <220> FEATURE:

143 <221> NAME/KEY: misc_feature

144 <222> LOCATION: (20)..(21)

145 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)

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W--> 148 cacugcagua ucuggccccc n 21

151 <210> SEQ ID NO: 5

152 <211> LENGTH: 21

153 <212> TYPE: DNA

154 <213> ORGANISM: Homo sapiens

157 <220> FEATURE:

158 <221> NAME/KEY: misc_feature

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159 <222> LOCATION: (20)..(21)
160 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)
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166 <210> SEQ ID NO: 6
167 <211> LENGTH: 21
168 <212> TYPE: DNA
169 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
174 <222> LOCATION: (20)..(21)
175 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)
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181 <210> SEQ ID NO: 7
182 <211> LENGTH: 21
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
187 <220> FEATURE:
188 <221> NAME/KEY: misc_feature
189 <222> LOCATION: (20)..(21)
190 <223> OTHER INFORMATION: Any "N" is a (2'-deoxy) thymidine. SI RNA Sequence (DNA/RNA)
192 <400> SEQUENCE: 7
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196 <210> SEQ ID NO: 8
197 <211> LENGTH: 745
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 8
203 Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
204 1 5 10 15
207 Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr
208 20 25 30
211 Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
212 35 40 45
215 Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
216 50 55 60
219 Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro
220 65 70 75 80
223 Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu
224 85 90 95
227 Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
228 100 105 110
231 Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
232 115 120 125
235 Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
236 130 135 140
239 Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile
240 145 150 155 160

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243 His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser
244           165           170           175
247 Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
248           180           185           190
251 Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly
252           195           200           205
255 Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His
256           210           215           220
259 Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys
260 225           230           235           240
263 Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser
264           245           250           255
267 His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met
268           260           265           270
271 Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly
272           275           280           285
275 Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met
276           290           295           300
279 Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser
280 305           310           315           320
283 Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser
284           325           330           335
287 Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln
288           340           345           350
291 Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala
292           355           360           365
295 Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val
296           370           375           380
299 Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser
300 385           390           395           400
303 Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile
304           405           410           415
307 Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His
308           420           425           430
311 Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln
312           435           440           445
315 Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys
316           450           455           460
319 Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu
320 465           470           475           480
323 Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu
324           485           490           495
327 Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys
328           500           505           510
331 Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly
332           515           520           525
335 Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Glu Leu
336           530           535           540
339 Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu

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340 545          550          555          560
343 Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser
344          565          570          575
347 Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His
348          580          585          590
351 Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu
352          595          600          605
355 Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys
356          610          615          620
359 Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met
360 625          630          635          640
363 Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile
364          645          650          655
367 Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu
368          660          665          670
371 Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala
372          675          680          685
375 Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu
376          690          695          700
379 Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu
380 705          710          715          720
383 Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met
384          725          730          735
387 Asn Leu Asp Trp Ser Trp Leu Thr Glu
388          740          745
391 <210> SEQ ID NO: 9
392 <211> LENGTH: 24
393 <212> TYPE: DNA
394 <213> ORGANISM: Homo sapiens
396 <400> SEQUENCE: 9
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400 <210> SEQ ID NO: 10
401 <211> LENGTH: 24
402 <212> TYPE: DNA
403 <213> ORGANISM: Homo sapiens
405 <400> SEQUENCE: 10
406 caacttgctc aaatgaccaa acag
409 <210> SEQ ID NO: 11
410 <211> LENGTH: 24
411 <212> TYPE: DNA
412 <213> ORGANISM: Homo sapiens
414 <400> SEQUENCE: 11
415 tgagcacacg gtctgactc tgca

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/730,614A

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Input Set : A:\9_263 seq list 10.25.04.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 20,21
Seq#:3; N Pos. 20,21
Seq#:4; N Pos. 20,21
Seq#:5; N Pos. 20,21
Seq#:6; N Pos. 20,21
Seq#:7; N Pos. 20,21

VERIFICATION SUMMARY

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Input Set : A:\9_263 seq list 10.25.04.ST25.txt

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L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0